



(1)

GENERAL INFORMATION:

- (i) APPLICANTS: Van der Bruggen, Pierre; Van den Eynde, Benoit; DeBacker, Olivier; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated, Polypeptides Which Bind to HLA-A29 Molecules, Nucleic Acid, The Molecules Encoding These, and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 31
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- (v) COMPUTER READABLE FORM:
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(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC
(D) SOFTWARE: Wordperfect
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- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCCGTCCG GACTCTTTTT CCTCTACTGA GATTCATCTG TGTGAAATAT 50
 GAGTTGGCGA GGAAGATCGA CCTATCGGCC TAGACCAAGA CGCTACGTAG 100
 AGCCTCCTGA AATGATTGGG CCTATGCGGC CCGAGCAGTT CAGTGATGAA 150
 GTGGAACCAG CAACACCTGA AGAAGGGGAA CCAGCAACTC AACGTCAGGA 200
 TCCTGCAGCT GCTCAGGAGG GAGAGGATGA GGGAGCATCT GCAGGTCAAG 250
 GGCCGAAGCC TGAAGCTGAT AGCCAGGAAC AGGGTCACCC ACAGACTGGG 300
 TGTGAGTGTG AAGATGGTCC TGATGGGCAG GAGATGGACC CGCCAAATCC 350
 AGAGGAGGTG AAAACGCCTG AAGAAGAGAT GAGGTCTCAC TATGTTGCCC 400
 AGACTGGGAT TCTCTGGCTT TTAATGAACA ATTGCTTCTT AAATCTTTCC 450
 CCACGGAAAC CTTGAGTGAC TGAAATATCA AATGGCGAGA GACCGTTTAG 500
 TTCCTATCAT CTGTGGCATG TGAAGGGCAA TCACAGTGTT AAAAGAAGAC 550
 ATGCTGAAAT GTTGCAGGCT GCTCCTATGT TGGAAAATTC TTCATTGAAG 600
 TTCTCCCAAT AAAGCTTTAC AGCCTTCTGC AAAGAAAAAA AAAAAA 646

- (2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

B2 AGACGCTACG TAGAGCCT 18

- (2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCAGGAC CATCTTCA 18

- (2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Arg Pro Arg Pro Arg Arg Tyr Val
 1 5

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- (2) INFORMATION FOR SEQ ID NO: 7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr Val
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Arg Pro Arg Pro Arg Arg Tyr Val Glu
 1 5

- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACCAAGACG CTACGTAG

18

- (2) INFORMATION FOR SEQ ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCATCAGGAC CATCTTCA

18

- br (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCGGCCCGAG CAGTTCA

17

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr Val Glu Pro Pro Glu Met Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACGCCAGGGA GCTGTGAGGC AGTGCTGTGT GGTTCCTGCC GTCCGGACTC 50
TTTTTCCTCT ACTGAGATTC ATCTGTGTGA AATATGAGTT GGCGAGGAAG 100
ATCGACCTAT CGGCCTAGAC CAAGACGCTA CGTAGAGCCT CCTGAAATGA 150
TTGGGCCTAT GCGGCCCGAG CAGTTCAGTG ATGAAGTGGA ACCAGCAACA 200
CCTGAAGAAG GGAACCAGC AACTCAACGT CAGGATCCTG CAGCTGCTCA 250
GGAGGGAGAG GATGAGGGAG CATCTGCAGG TCAAGGGCCG AAGCCTGAAG 300
CTCATAGCCA GGAACAGGGT CACCCACAGA CTGGGTGTGA GTGTGAAGAT 350
GGTCCTGATG GGCAGGAGAT GGACCCGCCA AATCCAGAGG AGGTGAAAAC 400
GCCTGAAGAA GGTGAAAAGC AATCACAGTG TTAAAAGAAG ACACGTTGAA 450
ATGATGCAGG CTGCTCCTAT GTTGGAAATT TGTTCATTAA AATTCTCCCA 500
ATAAAGCTTT ACAGCCTTCT GCAAAGAAAA AAAAAAAAAA 538

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCATATTTT ACACAGATGA GTTGGCGAGG AAGATCGACC TATTATTGGT 50
CTAGGCCAAT AATAGGTCGA TCTTCCTCGC CAACTCATAT TTCACACAGA 100
TGAATCTCAG TAGAGGAAAA TCGACCTATT ATTGGCCTAG ACCAAGGCGC 150
TATGTACAGC CTCCTGAAGT GATTGGGCCT ATGCGGCCCG AGCAGTTCAG 200
TGATGAAGTG GAACCAGCAA CACCTGAAGA AGGGGAACCA GCAACTCAAC 250

GTCAGGATCC TGCAGCTGCT CAGGAGGGAG AGGATGAGGG AGCATCTGCA 300
 GGTCAAGGGC CGAAGCCTGA AGCTGATAGC CAGGAACAGG GTCACCCACA 350
 GACTGGGTGT GAGTGTGAAG ATGGTCCTGA TGGGCAGGAG ATGGACCCGC 400
 CAAATCCAGA GGAGGTGAAA ACGCCTGAAG AAGGTGAAAA GCAATCACAG 450
 TGTTAAAAGA AGGCACGTTG AAATGATGCA GGCTGCTCCT ATGTTGGAAA 500
 TTTGTTTCATT AAAATTCTCC CAATAAAGCT TTACAGCCTT CTGCAAAGAA 550
 AAAAAAAAAA 560

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGCCAGGGAG CTGTGAGGCA GTGCTGTGTG GTTCCTGCCG TCCGGACTCT 50
 TTTTCCTCTA CTGAGATTCA TCTGTGTGAA ATATGAGTTG GCGAGGAAGA 100
 TCGACCTATT ATTGGCCTAG ACCAAGGCGC TATGTACAGC CTCCTGAAAT 150
 GATTGGGCCT ATGCGGCCCC AGCAGTTCAG TGATGAAGTG GAACCAGCAA 200
 CACCTGAAGA AGGGGAACCA GCAACTCAAC GTCAGGATCC TGCAGCTGCT 250
 CAGGAGGGAG AGGATGAGGG AGCATCTGCA GGTCAAGGGC CGAAGCCTGA 300
 AGCTGATAGC CAGGAACAGG GTCACCCACA GACTGGGTGT GAGTGTGAAG 350
 ATGGTCCTGA TGGGCAGGAG ATGGACCCGC CAAATCCAGA GGAGGTGAAA 400
 ACGCCTGAAG AAGGTGAAAA GCAATCACAG TGTTAAAAGA AGGCACGTTG 450
 AAATGATGCA GGCTGCTCCT ATGTTGGAAA TTTGTTTCATT AAAATTCTCC 500
 CAATAAAGCT TTACAGCCTT CTGCAAAAAA AAAAAAAAAA 540

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AGCTGTGAGG CAGTGCTGTG TGGTTCCTGC CGTCCGGA CTCTTTTCCTC 50
TACTGAGATT CATCTGTGTG AAATATGAGT TGGCGAGGAA GATCGACCTA 100
TTATTGGCCT AGACCAAGGC GCTATGTACA GCCTCCTGAA GTGATTGGGC 150
CTATGCGGCC CGAGCAGTTC AGTGATGAAG TGAACACAGC AACACCTGAA 200
GAAGGGGAAC CAGCAACTCA ACGTCAGGAT CCTGCAGCTG CTCAGGAGGG 250
AGAGGATGAG GGAGCATCTG CAGGTCAAGG GCCGAAGCCT GAAGCTGATA 300
GCCAGGAACA GGGTCACCCA CAGACTGGGT GTGAGTGTGA AGATGGTCCT 350
GATGGGCAGG AGATGGACCC GCCAAATCCA GAGGAGGTGA AAACGCCTGA 400
AGAAGGTGAA AAGCAATCAC AGTGTTAAAA GAAGGCACGT TGAAATGATG 450
CAGGCTGCTC CTATGTTGGA AATTTGTTCA TAAAATTCT CCAATAAAG 500
CTTTACAGCC TTCTGCAAAG AAAAAAAAAA AA 532

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT 50
TTTCCTCTAC TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT 100
CGACCTATTA TTGGCCTAGA CCAAGGCGCT ATGTACAGCC TCCTGAAGTG 150
ATTGGGCCTA TGCGGCCCGA GCAGTTCAGT GATGAAGTGG AACCAGCAAC 200
ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT GCAGCTGCTC 250

AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA 350
 TGGTCCTGAT GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA 400
 CGCCTGAAGA AGGTGAAAAG CAATCACAGT GTTAAAAGAA GACACGTTGA 450
 AATGATGCAG GCTGCTCCTA TGTTGGAAAT TTGTTCATTA AAATTCTCCC 500
 AATAAAGCTT TACAGCCTTC TGCAAAAAAA AAAAAAAA 539

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCATGAG GTATTTC

17

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTTCACCACA TGCGTGT

17

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg Tyr Val Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Tyr Tyr Trp Pro Arg Pro Arg Arg Tyr

1

5

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Each Xaa may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Xaa Xaa Trp Pro Xaa Xaa Xaa Xaa Tyr

1

5

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Each Xaa may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Xaa Xaa Trp Xaa Arg Xaa Xaa Xaa Tyr

1

5

32
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- (2) INFORMATION FOR SEQ ID NO: 25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Each Xaa may be any amino acid
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Xaa Xaa Trp Xaa Xaa Xaa Xaa Arg Tyr
 1 5

B2

- (2) INFORMATION FOR SEQ ID NO: 26:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: protein
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
 1 5 10 15
 Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser
 20 25 30
 Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln
 35 40 45
 Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser
 50 55 60
 Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
 65 70 75 80
 Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
 85 90 95
 Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg
 100 105 110
 Ser His Tyr Val Ala Gln Thr Gly Ile Leu Trp Leu Leu Met Asn Asn
 115 120 125
 Cys Phe Leu Asn Leu Ser Pro Arg Lys Pro
 130 135

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 T08050-54728460

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5 10 15
Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser
20 25 30
Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln
35 40 45
Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser
50 55 60
Ala Gly Gln Gly Pro Lys Pro Glu Ala His Ser Gln Glu Gln Gly His
65 70 75 80
Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
85 90 95
Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu Lys
100 105 110
Gln Ser Gln Cys
115

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Asn Leu Ser Arg Gly Lys Ser Thr Tyr Tyr Trp Pro Arg Pro Arg
1 5 10 15
Arg Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln
20 25 30
Phe Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala
35 40 45
Thr Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly
50 55 60
Ala Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln
65 70 75 80
Gly His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln
85 90 95

Glu Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly
 100 105 110
 Glu Lys Gln Ser Gln Cys
 115

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
 1 5 10 15
 Tyr Val Gln Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe
 20 25 30
 Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
 35 40 45
 Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
 50 55 60
 Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
 65 70 75 80
 His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
 85 90 95
 Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
 100 105 110
 Lys Gln Ser Gln Cys
 115

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
 1 5 10 15
 Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe
 20 25 30
 Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
 35 40 45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
 50 55 60
 Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
 65 70 75 80
 His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
 85 90 95
 Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
 100 105 110
 Lys Gln Ser Gln Cys
 115

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg
 1 5 10 15
 Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe
 20 25 30
 Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr
 35 40 45
 Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala
 50 55 60
 Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly
 65 70 75 80
 His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu
 85 90 95
 Val Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu
 100 105 110
 Lys Gln Ser Gln Cys
 115